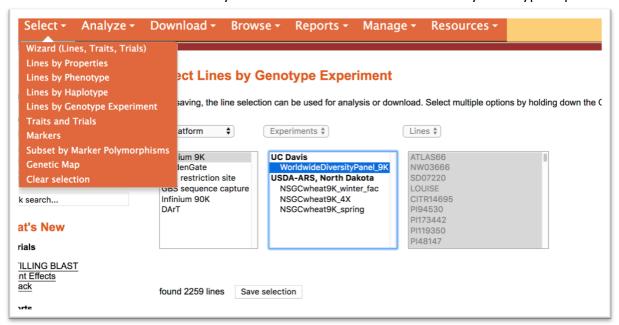R Script is a programming language widely used among statisticians, data miners, and data analysis. The software is available from CRAN Download R and Microsoft R Open. Data from T3 can be accessed by
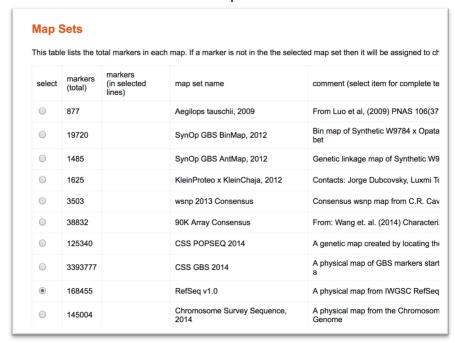
1. Saving from T3 then reading into R
2. Using BrAPI R package to read directly into R
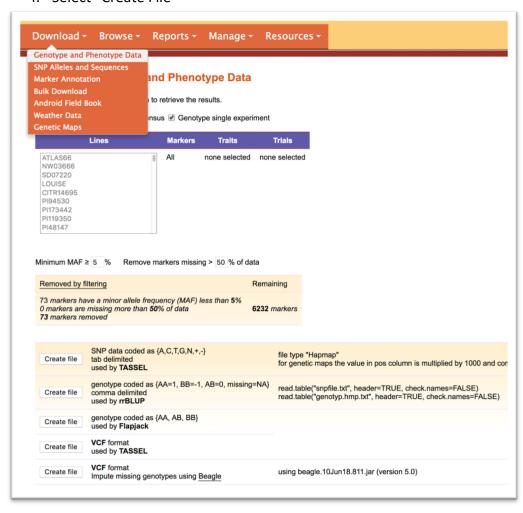
Download data from T3 website then read into R

1. The data can be selected by Select => Wizard or Select => Lines by Genotype Experiment

2. Go to Select => Genetic Map

3. Go to Download => Genotype and Phenotype Data - Select rrBLUP format
4. Select "Create File"

5. In the R script read in file

```
R version 3.5.0 (2018-04-23) -- "Joy in Playing"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-apple-darwin15.6.0 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
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  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> snp <- read.table("genotype.hmp.txt", header=TRUE, check.names=FALSE)
> str(snp)
'data.frame':   6232 obs. of  2263 variables:
 $ rs                        : Factor w/ 6232 levels "IWA1","IWA100",..: 1 2 3 4 5 6 7 8 9 10 ..
 $ alleles                   : Factor w/ 4 levels "A/C","A/G","T/C",..: 2 3 3 2 2 1 3 3 3 3 ...
 $ chrom                     : Factor w/ 23 levels "1A","1B","1D",..: 13 20 16 2 11 11 4 4 10 4
 $ pos                       : int  588550278 457383441 606767942 542431643 552018214 552018152
 $ ATLAS66                   : int  1 1 1 1 1 1 1 -1 1 -1 ...
 $ NW03666                   : int  1 1 -1 1 1 1 1 -1 1 -1 ...
 $ SD07220                   : int  1 1 -1 -1 1 1 1 -1 1 -1 ...
 $ LOUISE                    : int  -1 1 1 -1 -1 -1 1 -1 1 -1 ...
 $ CITR14695                 : int  1 1 -1 1 -1 -1 1 -1 -1 -1 ...
 $ PI94530                   : int  -1 1 -1 -1 -1 -1 1 -1 1 -1 ...
 $ PI173442                  : int  1 -1 -1 1 -1 -1 -1 1 1 1 ...
 $ PI119350                  : int  -1 1 1 1 -1 -1 1 -1 1 -1 ...
```

Use BrAPI R package to directly read data from T3 in R

The documentation for this package is at https://github.com/CIP-RIU/brapi. The current package (Aug 1, 2018) will direct you to t3sandbox.org. This will be fixed soon to point to triticaetoolbox.org/wheat.

In R execute
```
install.packages("devtools")
devtools::install_github("CIP-RIU/brapi")

library(brapi)
library(magrittr)

t3wheat <= ba_db()$t3s

list available calls
bp_calls(t3wheat)
```